

APPROVED	U.G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

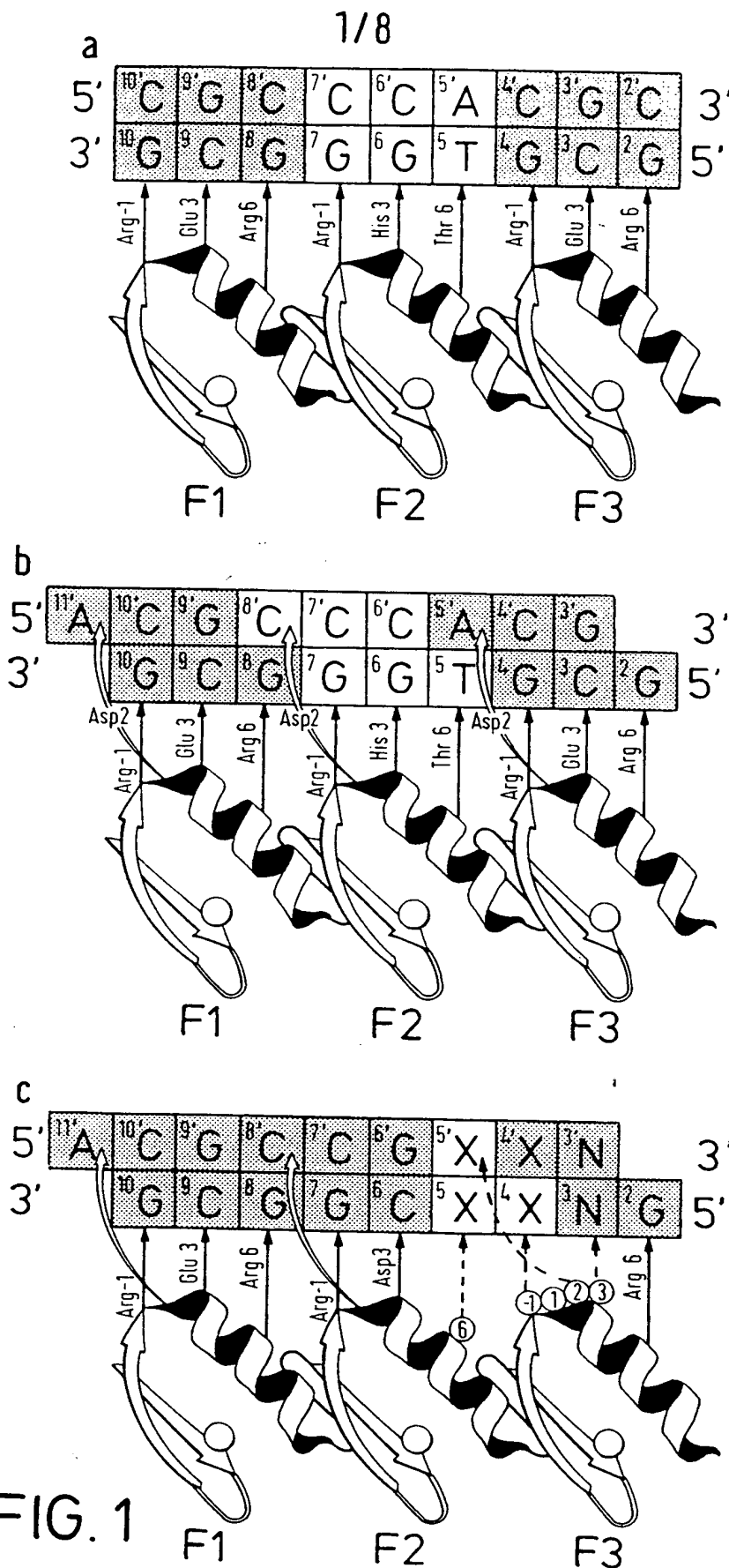


FIG. 1

SUBSTITUTE SHEET (RULE 26)

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[illegible][illegible]

FIG. 2

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O.G. FIG.	CLASS	SUBCLASS
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BASE AT POSITIONS 4'X AND 5'X OF DNA SITES USED IN SELECTIONS	AMINO ACIDS SELECTED IN FINGERS 2 AND 3		BINDING SITE SIGNATURE		No. OF CLONES SELECTED AND SCREENED	BASES AT POSITIONS 4'X AND 5'X OF DNA SITES USED IN SELECTIONS	AMINO ACIDS SELECTED IN FINGERS 2 AND 3		BINDING SITE SIGNATURE		No. OF CLONES SELECTED AND SCREENED		
	F2	F3	4'X	5'X			F2	F3	4'X	5'X			
GG	6	-1123	G A T C	G A T C	4	CC	6	-1123	G A T C	G A T C	1		
	R	RLEY			4		T	DPHN			4		
	*R	RSED			1		E	HSKS			1		
	R	RHTH			1		E	HRQN			1		
	R	RSSE			1		S	DRAN			1		
	R	RSSA			1		T	DRAN			2		
AG	R	QVTT			4	AC	*Y	RSQD			3		
	*R	QSGD			5		V	QVGH			2		
	R	QLAT			2		T	QLAT			3		
	R	QDAH			1		TA	N	TSQA			4	
	R	QRAS			1			N	TSAS			2	
	K	QSTS			1			K	LAQT			1	
TG	R	SSGD			1	*E		RSRD			3		
	R	SASA			1	E		RLRD			4		
	*R	NSGD			1	V		HLAT			1		
	R	LVQN			1	V	HLTT			1			
	K	TGAS			1	L	VGHH			1			
	R	TPSG			1	CA	Y	HPAT			2		
R	TQTA			1	N		HPAN			1			
R	TSAA			2	E		HMSN			9			
CG	R	DTSV			3		L	DSRA			2		
	R	DAST			2		GT	*T	KSSD			2	
	R	DASA			1			*K	SSSD			1	
	R	DTSS			2	*K		RSHD			1		
	GC	A	RNHD			2		A	RSSY			1	
		*N	RSTD			3		T	RSSS			1	
*S		RSTD			6	T		RKTD			1		
S		SRHS			1	AT	S	QIST			3		
T		RNST			1		S	QIGA			1		
T		RTST			1		T	QYST			1		
T	TRYs			3	T		QSAS			1			
T	RAQN			1	T		QSQH ¹			1			
AC	A	QAAT			4		T	QTSH			1		
	A	QGTN			1	T	QPGH			1			
	*V	TSRD			4	T	QDTT			1			
	S	QRGA			1	K	QDST			2			
	S	QSTT			2	TT	T	TAST			1		
	A	TSSS			1		T	TASH			1		
T	SSST			1	T		TSSV			1			
TC	D	TISN			1		T	TSSA			1		
	N	TSTA			1		S	HHTS			1		
	V	TSSL			4		S	HAQT			1		
	V	TSSI			1	S	HATT			4			
	V	TSNS			3	CT	K	DHSS			5		
	*R	GSND			1		T	HPST			1		
A	TTSS			1	S		DSSR			1			
T	TAGS			1	CT		T	HPST			1		
S	TTSS			1			S	DSSR			1		
S	TSSA			1			CT	T	HPST			1	
S	LSTT			1		S		DSSR			1		
G	LSST			1		CT		T	HPST			1	
TC	D	TISN						1	S	DSSR			1
	N	TSTA			1			CT	T	HPST			1
	V	TSSL			4				S	DSSR			1
	V	TSSI			1		CT		T	HPST			1
	V	TSNS			3				S	DSSR			1
	*R	GSND			1	CT			T	HPST			1
A	TTSS			1	S				DSSR			1	
T	TAGS			1	CT			T	HPST			1	
S	TTSS			1				S	DSSR			1	
S	TSSA			1			CT	T	HPST			1	
S	LSTT			1				S	DSSR			1	
G	LSST			1		CT		T	HPST			1	
TC	D	TISN						1	S	DSSR			1
	N	TSTA			1			CT	T	HPST			1
	V	TSSL			4				S	DSSR			1
	V	TSSI			1		CT		T	HPST			1
	V	TSNS			3				S	DSSR			1
	*R	GSND			1	CT			T	HPST			1
A	TTSS			1	S				DSSR			1	
T	TAGS			1	CT			T	HPST			1	
S	TTSS			1				S	DSSR			1	
S	TSSA			1			CT	T	HPST			1	
S	LSTT			1				S	DSSR			1	
G	LSST			1		CT		T	HPST			1	
TC	D	TISN						1	S	DSSR			1
	N	TSTA			1			CT	T	HPST			1
	V	TSSL			4				S	DSSR			1
	V	TSSI			1		CT		T	HPST			1
	V	TSNS			3				S	DSSR			1
	*R	GSND			1	CT			T	HPST			1
A	TTSS			1	S				DSSR			1	
T	TAGS			1	CT			T	HPST			1	
S	TTSS			1				S	DSSR			1	
S	TSSA			1			CT	T	HPST			1	
S	LSTT			1				S	DSSR			1	
G	LSST			1		CT		T	HPST			1	
TC	D	TISN						1	S	DSSR			1
	N	TSTA			1			CT	T	HPST			1
	V	TSSL			4				S	DSSR			1
	V	TSSI			1		CT		T	HPST			1
	V	TSNS			3				S	DSSR			1
	*R	GSND			1	CT			T	HPST			1
A	TTSS			1	S				DSSR			1	
T	TAGS			1	CT			T	HPST			1	
S	TTSS			1				S	DSSR			1	
S	TSSA			1			CT	T	HPST			1	
S	LSTT			1				S	DSSR				

RELATIVE SIGNATURE STRENGTH ■ ≤1.00 ■ 0.80 ■ 0.60 ■ 0.40 ■ 0.20 □ 0.00

FIG. 3
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APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

a

AMINO ACID SELECTED AT POSITION -1

BASE PRESENT AT POSITION ⁴ X IN BINDING SIGNATURES	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
G	0	0	0	0	0	0	0	0	1	0	0	0	0	0	16	2	2	0	0	0
A	0	0	0	0	0	0	0	0	0	0	0	0	0	21	1	1	1	0	0	0
T	0	0	0	0	0	1	7	0	0	4	0	1	0	2	5	3	21	1	0	0
C	0	0	10	0	0	0	7	0	0	2	0	0	0	0	2	0	0	0	0	0

↓ ↓ ↓ ↓ ↓

C T/C T A G(T) T

RECOGNITION PATTERNS

b

AMINO ACID SELECTED AT POSITION 6

BASE PRESENT AT POSITION ⁵ X IN BINDING SIGNATURES	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
G	0	0	0	0	0	0	0	0	4	1	0	0	0	0	21	0	0	0	0	0
A	0	0	0	3	0	0	0	0	1	2	0	3	0	0	0	0	2	3	0	2
T	1	0	0	0	0	1	0	0	5	0	0	0	0	0	0	10	17	3	0	0
C	5	0	1	3	0	1	0	0	0	0	0	3	0	0	2	12	14	6	0	0

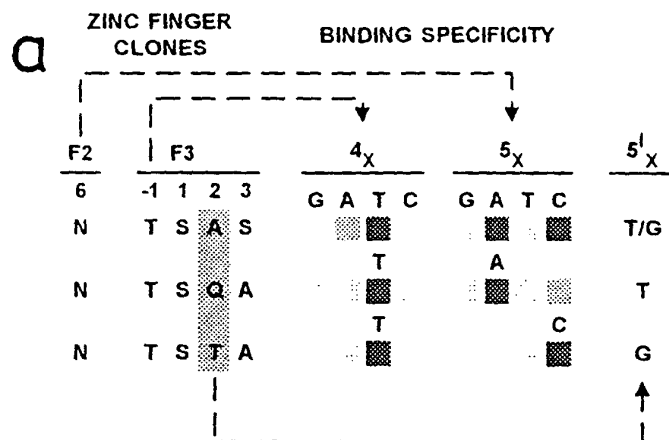
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C A/C G/T A/C G T/C C(A/T)

RECOGNITION PATTERNS

FIG. 4

O.G. FIG.	CLASS	SUBCLASS
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b

AMINO ACID SELECTED AT POSITION 2	ZINC FINGER CLONES					CROSS-STRAND BINDING SPECIFICITY	No. OF CLONES SELECTED AND SCREENED
	F2	F3				5' _X	
	6	-1	1	2	3	G A T C	
E	R	R	L	E	Y		4
	R	R	S	E	D		4
N	V	T	S	N	S		3
	R	G	S	N	D		1
Q	Y	R	S	Q	D		3
	N	T	S	Q	A		4
	K	L	A	Q	T		1
	T	R	A	Q	N		1
	E	H	R	Q	N		1
	S	H	A	Q	T		1
R	L	D	S	R	A		2
	E	R	S	R	D		3
	E	R	L	R	D		4
	V	T	S	R	D		4
H	A	R	N	H	D		2
	S	S	R	H	S		1
	T	D	P	H	N		1
K	E	H	S	K	S		4

FIG. 5

FIG. 6A

	8	9	10	11	12	13	14	15	16
Wild-type	5' GTG	GTG	GGC	CCC	GGC	GGT	GTG	GGC	AAG 3'
	3' CAC	CAC	CCG	CGG	CCG	CCA	CAC	CCG	TTG 5'

EJ mutant

F1	M	A	E	K	P	F	Q	C	R	I	C	M	R	N	F	S	D	R	S	S	L	T	R	H	T	R	T	H	T	C	E	K	P
F2						F	Q	C	R	I	C	M	R	N	F	S	D	R	S	S	L	T	R	H	T	R	T	H	T	C	E	K	P
F3						F	Q	C	R	I	C	M	R	N	F	S	D	R	S	S	L	T	R	H	T	R	T	H	T	C	E	K	P

FIG. 6C

 α - helix

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B

APPROVED	O.G. FIG.
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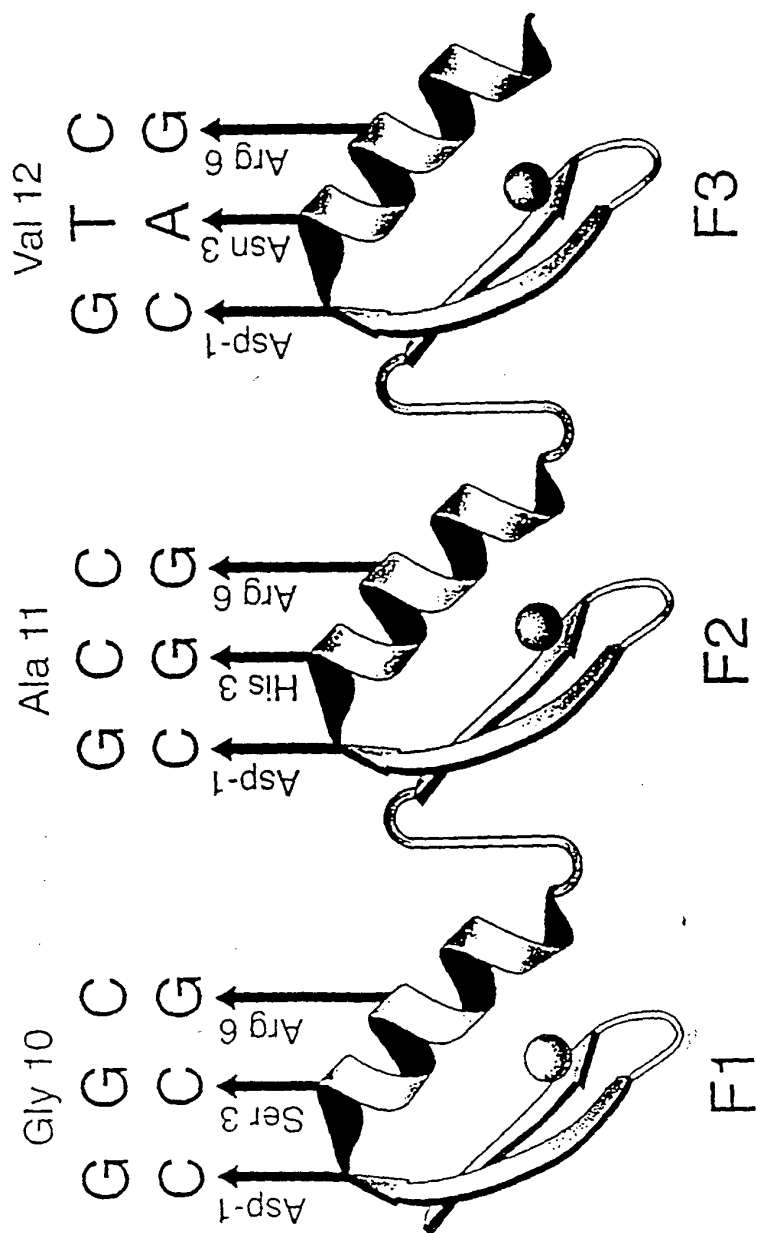


FIG. 6B

APPROVED BY DRAFTSMAN	O.C. FIG.	
	CLASS	SUBCLASS

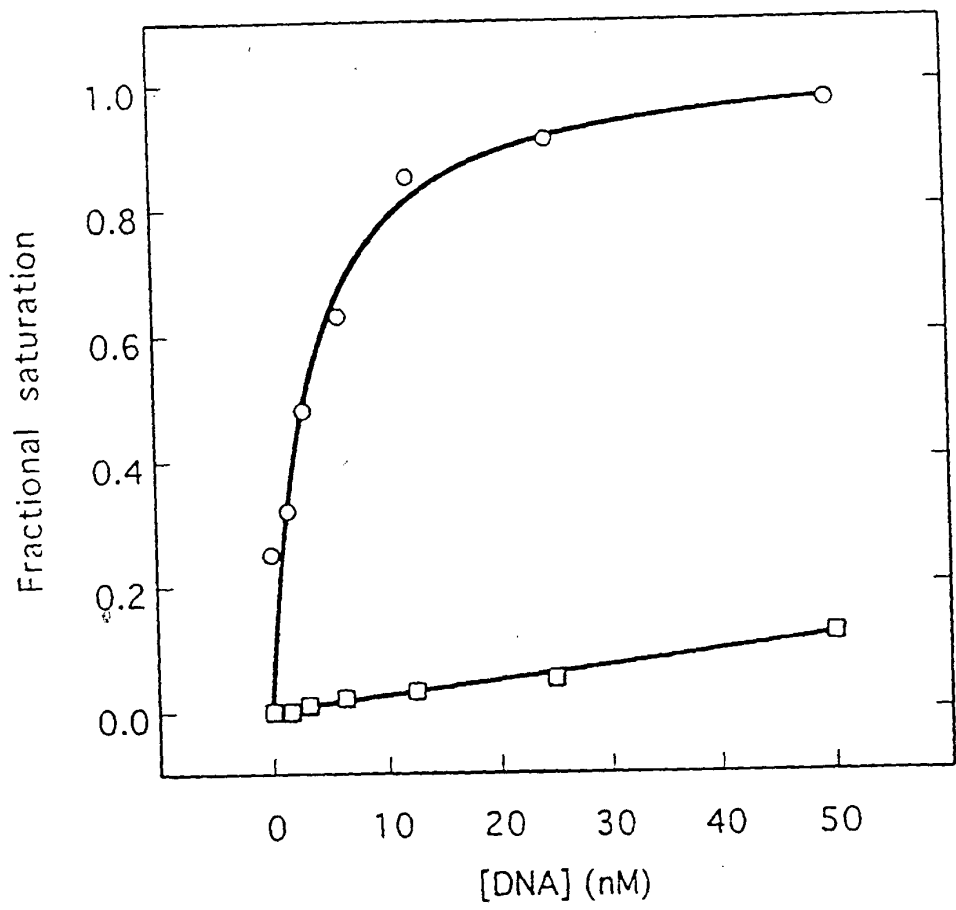


FIG. 7

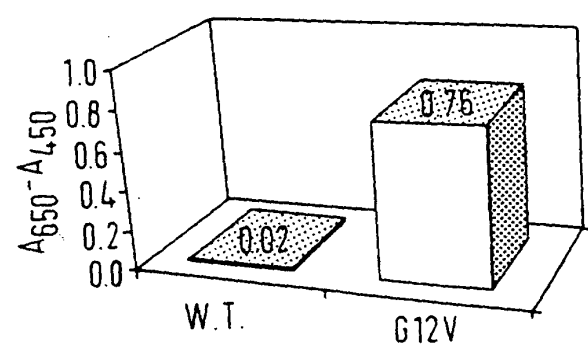


FIG. 8